

Atty Dkt No. 9000-0055
PATENT

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Patricia K. Hingabe
(Typed or Printed Name of Person Mailing Paper or Fee)

Patricia K. Hingabe
(Signature of Person Mailing Paper or Fee)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In Re Application of:

BOLTON et al.

Serial No.: Unassigned

Group Art Unit: Unassigned

Filing Date: Filed Herewith

Examiner: Unassigned

Title: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST
STREPTOCOCCUS INFECTION

STATEMENT TO SUPPORT FILING AND SUBMISSION IN ACCORDANCE
WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

The undersigned hereby states that the content of the attached papers and the computer-readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. §§ 1.821(c) and (e), respectively, are the same.

Respectfully submitted,

Date: 6/11/01

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Roberta L. Robins
Registration No. 33,208

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Menlo Park, CA 94025
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SEQUENCE LISTING

<110> Bolton, Alexandra J.
Perez-Casal, Jose
Fontaine, Michael
Potter, Andrew A.

<120> IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST
STREPTOCOCCUS INFECTION

<130> 9000-0055

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<170> PatentIn Ver. 2.0

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<213> Artificial Sequence

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<213> Artificial Sequence

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<212> DNA

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<221> CDS

<222> (1)..(1011)

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gca ttc cgt cgt att caa aat gtt gaa ggt gtt gaa gta act cgt atc	96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile	
20 25 30	
aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tac gat	144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
35 40 45	
aca act caa gga cgt ttt gac gga act gtt gaa gtt aaa gaa ggt gga	192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly	
50 55 60	
ttt gaa gta aac gga aac ttc atc aaa gtt tct gct gaa cgt gat cca	240
Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro	
65 70 75 80	
gaa aac atc gac tgg gca act gac ggt gtt gaa atc gtt ctg gaa gca	288
Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala	
85 90 95	
act ggt ttc ttt gct aaa aaa gaa gct gct gaa aaa cac tta cat gct	336
Thr Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala	
100 105 110	
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Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val	
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Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
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Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
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Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr	
165 170 175	
aca atc cac gct tat act ggt gac caa atg atc ctt gac gga cca cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gct gca aac att gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val	
195 200 205	

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Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
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gga tca gta act gag ttg gtt gta act ctt gat aaa aac gtt tct gtt	768
Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val	
245 250 255	
gac gaa atc aac gct gct atg aaa gct gct tca aac gac agt ttc ggt	816
Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly	
260 265 270	
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Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr	
275 280 285	
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Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly	
290 295 300	
tca caa ttg gtt aaa gtt gta tca tgg tat gac aat gaa atg tct tac	960
Ser Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
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taa	1011

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<212> PRT

<213> Streptococcus dysgalactiae

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35 40 45

Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
50 55 60

Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro
 65 70 75 80
 Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
 85 90 95
 Thr Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala
 100 105 110
 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
 115 120 125
 Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
 130 135 140
 Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
 145 150 155 160
 Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr
 165 170 175
 Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
 180 185 190
 Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
 195 200 205
 Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
 210 215 220
 Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
 225 230 235 240
 Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val
 245 250 255
 Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly
 260 265 270
 Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr
 275 280 285
 Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly
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 Ser Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
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<212> DNA

<213> Streptococcus agalactiae

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<222> (1)..(1011)

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Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
20 25 30

aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tat gac 144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
35 40 45

aca act caa ggt cgt ttc gac ggt act gtt gaa gtt aaa gaa ggt gga 192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
50 55 60

ttc gaa gtt aac ggt caa ttt gtt aaa gtt tct gct gaa cgc gaa cca 240
Phe Glu Val Asn Gly Gln Phe Val Lys Val Ser Ala Glu Arg Glu Pro
65 70 75 80

gca aac att gac tgg gct act gat ggc gta gaa atc gtt ctt gaa gca 288
Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
85 90 95

act ggt ttc ttt gca tca aaa gaa aaa gct gga caa cac atc cat gaa 336
Thr Gly Phe Phe Ala Ser Lys Glu Lys Ala Gly Gln His Ile His Glu
100 105 110

aat ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt 384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
115 120 125

aaa aca gtt gtt ttc aac act aac cac gat atc ctt gat gga act gaa 432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
130 135 140

aca gtt atc tca ggt gct tca tgt act aca aac tgt ctt gct cca atg 480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145 150 155 160

gct aaa gct tta caa gac aac ttt ggt gtt aaa caa ggt ttg atg act 528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
165 170 175

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Asn	Asp	Leu	Thr	Asp	Pro	Asn	Met	Leu	Ala	His	Leu	Leu	Lys	Tyr	Asp	35	40	45	
Thr	Thr	Gln	Gly	Arg	Phe	Asp	Gly	Thr	Val	Glu	Val	Lys	Glu	Gly	Gly	50	55	60	
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Thr	Gly	Phe	Phe	Ala	Ser	Lys	Glu	Lys	Ala	Gly	Gln	His	Ile	His	Glu	100	105	110	
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Lys	Thr	Val	Val	Phe	Asn	Thr	Asn	His	Asp	Ile	Leu	Asp	Gly	Thr	Glu	130	135	140	
Thr	Val	Ile	Ser	Gly	Ala	Ser	Cys	Thr	Thr	Asn	Cys	Leu	Ala	Pro	Met	145	150	155	160
Ala	Lys	Ala	Leu	Gln	Asp	Asn	Phe	Gly	Val	Lys	Gln	Gly	Leu	Met	Thr	165	170	175	
Thr	Ile	His	Ala	Tyr	Thr	Gly	Asp	Gln	Met	Ile	Leu	Asp	Gly	Pro	His	180	185	190	
Arg	Gly	Gly	Asp	Leu	Arg	Arg	Ala	Arg	Ala	Gly	Ala	Ala	Asn	Ile	Val	195	200	205	
Pro	Asn	Ser	Thr	Gly	Ala	Ala	Lys	Ala	Ile	Gly	Leu	Val	Ile	Pro	Glu	210	215	220	
Leu	Asn	Gly	Lys	Leu	Asp	Gly	Ala	Ala	Gln	Arg	Val	Pro	Val	Pro	Thr	225	230	235	240
Gly	Ser	Val	Thr	Glu	Leu	Val	Ala	Thr	Leu	Glu	Lys	Asp	Val	Thr	Val	245	250	255	
Glu	Glu	Val	Asn	Ala	Ala	Met	Lys	Ala	Ala	Ala	Asn	Asp	Ser	Tyr	Gly	260	265	270	
Tyr	Thr	Glu	Asp	Pro	Ile	Val	Ser	Ser	Asp	Ile	Val	Gly	Ile	Ser	Tyr	275	280	285	
Gly	Ser	Leu	Phe	Asp	Ala	Thr	Gln	Thr	Lys	Val	Gln	Thr	Val	Asp	Gly	290	295	300	

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Thr Ser Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
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<212> DNA

<213> Streptococcus uberis

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 Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
 20 25 30

aac gat ctt act gac cca aat atg ctt gca cac ttg ttg aaa tat gat 144
 Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
 35 40 45

aca act caa ggt cgt ttc gac ggt aca gtt gaa gtt aaa gat ggt gga 192
 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
 50 55 60

ttc gaa gtt aac gga aac ttc atc aaa gtt tct gct gaa aaa gat cca 240
 Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Lys Asp Pro
 65 70 75 80

gaa aac att gac tgg gca act gac ggt gta gaa atc gtt ctt gaa gca 288
 Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
 85 90 95

act ggt ttc ttt gct aaa aaa gca gct gct gaa aaa cat tta cat gct 336
 Thr Gly Phe Phe Ala Lys Lys Ala Ala Ala Glu Lys His Leu His Ala
 100 105 110

aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga gat gat gtt 384
 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val
 115 120 125

aaa act gtt gta ttt aac aca aac cat gac att ctt gac ggt aca gaa 432
 Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
 130 135 140

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Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gct ttg caa gat aac ttt ggt gtt aaa caa ggt ttg atg aca	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
165 170 175	
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Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gca agc aac att gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ser Asn Ile Val	
195 200 205	
cct aac tca act ggt gct gct aaa gca atc ggt ctt gta atc cca gaa	672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
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tta aat ggt aaa ctt gac ggt gct gca caa cgt gtt cct gtt cca act	720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
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gga tca gta act gaa tta gta gca gtt ctt gaa aaa gaa act tca gtt	768
Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Glu Thr Ser Val	
245 250 255	
gaa gaa atc aac gca gca atg aaa gca gct gca aac gat tca tac gga	816
Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Asn Asp Ser Tyr Gly	
260 265 270	
tac act gaa gac cca atc gta tct tct gat atc atc ggt atg gct tac	864
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Ile Gly Met Ala Tyr	
275 280 285	
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Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly	
290 295 300	
aat caa tta gtt aaa gtt gtt tca tgg tat gac aac gaa atg tct tac	960
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
305 310 315 320	
act gca caa ctt gtt cgt act ctt gag tac ttt gca aaa atc gct aaa	1008
Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys	
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taa	1011
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<212> PRT

<213> Streptococcus uberis

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35 40 45
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
50 55 60
Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Lys Asp Pro
65 70 75 80
Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
85 90 95
Thr Gly Phe Phe Ala Lys Lys Ala Ala Glu Lys His Leu His Ala
100 105 110
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val
115 120 125
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
130 135 140
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145 150 155 160
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
165 170 175
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
180 185 190
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ser Asn Ile Val
195 200 205
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
210 215 220
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
225 230 235 240
Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Glu Thr Ser Val
245 250 255
Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
260 265 270

Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Ile Gly Met Ala Tyr
 275 280 285
 Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
 290 295 300
 Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
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 Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
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 gct ttc cgt cgt att caa aat gta gaa ggt gtt gaa gtt act cgc atc 96
 Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
 20 25 30
 aac gac ctt aca gat cca aat atg ctt gca cac ttg tta aaa tac gat 144
 Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
 35 40 45
 aca act caa ggt cgt ttt gac ggt act gta gaa gtt aaa gat ggt gga 192
 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
 50 55 60
 ttt gac gtt aac gga aaa ttc att aaa gtt tct gct gaa aaa gat cca 240
 Phe Asp Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Lys Asp Pro
 65 70 75 80
 gaa caa att gac tgg gca act gac ggt gtt gaa atc gtt ctt gaa gca 288
 Glu Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
 85 90 95
 act ggt ttc ttt gct aaa aaa gca gct gct gaa aaa cat tta cat gaa 336
 Thr Gly Phe Phe Ala Lys Lys Ala Ala Ala Glu Lys His Leu His Glu
 100 105 110
 aat ggt gct aaa aaa gtt gtt atc act gct cct ggt gga gat gac gtg 384
 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val
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Asn	Asp	Leu	Thr	Asp	Pro	Asn	Met	Leu	Ala	His	Leu	Leu	Lys	Tyr	Asp
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Thr	Thr	Gln	Gly	Arg	Phe	Asp	Gly	Thr	Val	Glu	Val	Lys	Asp	Gly	Gly
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Phe	Asp	Val	Asn	Gly	Lys	Phe	Ile	Lys	Val	Ser	Ala	Glu	Lys	Asp	Pro
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Glu	Gln	Ile	Asp	Trp	Ala	Thr	Asp	Gly	Val	Glu	Ile	Val	Leu	Glu	Ala
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Thr	Gly	Phe	Phe	Ala	Lys	Lys	Ala	Ala	Ala	Glu	Lys	His	Leu	His	Glu
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Lys	Thr	Val	Val	Phe	Asn	Thr	Asn	His	Asp	Ile	Leu	Asp	Gly	Thr	Glu
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145					150					155					160
Ala	Lys	Ala	Leu	Gln	Asp	Asn	Phe	Gly	Val	Lys	Gln	Gly	Leu	Met	Thr
			165						170					175	
Thr	Ile	His	Ala	Tyr	Thr	Gly	Asp	Gln	Met	Leu	Leu	Asp	Gly	Pro	His
			180					185					190		
Arg	Gly	Gly	Asp	Leu	Arg	Arg	Ala	Arg	Ala	Gly	Ala	Asn	Asn	Ile	Val
		195					200					205			
Pro	Asn	Ser	Thr	Gly	Ala	Ala	Lys	Ala	Ile	Gly	Leu	Val	Ile	Pro	Glu
	210					215					220				
Leu	Asn	Gly	Lys	Leu	Asp	Gly	Ala	Ala	Gln	Arg	Val	Pro	Val	Pro	Thr
225					230					235					240
Gly	Ser	Val	Thr	Glu	Leu	Val	Ala	Val	Leu	Asn	Lys	Glu	Thr	Ser	Val
				245					250					255	

Glu Glu Ile Asn Ser Val Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
260 265 270

Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Phe
275 280 285

Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
290 295 300

Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
305 310 315 320

Thr Ala Gln Leu Asp Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
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<212> DNA
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<220>
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gca ttc cgt cgt att caa aat gtt gaa ggt gtt gaa gta act cgt atc 96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
20 25 30

aat gac ctt aca gat cct aac atg ctt gca cac ttg ttg aaa tat gat 144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
35 40 45

aca act caa ggt cgt ttt gac ggt aca gtt gaa gtt aaa gat ggt gga 192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
50 55 60

ttc gaa gtt aac gga agc ttt gtt aaa gtt tct gca gaa cgc gaa cca 240
Phe Glu Val Asn Gly Ser Phe Val Lys Val Ser Ala Glu Arg Glu Pro
65 70 75 80

gca aac att gac tgg gct act gat ggt gta gac atc gtt ctt gaa gca 288
Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Asp Ile Val Leu Glu Ala
85 90 95

aca ggt ttc ttc gct tct aaa gca gct gct gaa caa cac att cac gct 336
Thr Gly Phe Phe Ala Ser Lys Ala Ala Ala Glu Gln His Ile His Ala
100 105 110

aac Asn	ggt Gly	gcg Ala	aaa Lys	aaa Lys	gtt Val	gtt Val	atc Ile	aca Thr	gct Ala	cct Pro	ggt Gly	gga Gly	aat Asn	gac Asp	gtt Val	384
115						120			125							
aaa Lys	aca Thr	gtt Val	gtt Val	tac Tyr	aac Asn	act Thr	aac Asn	cat His	gat Asp	att Ile	ctt Leu	gat Asp	gga Gly	act Thr	gaa Glu	432
130						135			140							
aca Thr	gtt Val	atc Ile	tca Ser	ggt Gly	gct Ala	tca Ser	tgt Cys	act Thr	aca Thr	aac Asn	tgt Cys	tta Leu	gct Ala	cca Pro	atg Met	480
145			150						155			160				
gct Ala	aaa Lys	gca Ala	tta Leu	caa Gln	gat Asp	aac Asn	ttt Phe	ggt Gly	gta Val	aaa Lys	caa Gln	ggt Gly	tta Leu	atg Met	act Thr	528
			165						170			175				
act Thr	atc Ile	cat His	ggt Gly	tac Tyr	act Thr	ggt Gly	gac Asp	caa Gln	atg Met	gtt Val	ctt Leu	gac Asp	gga Gly	cca Pro	cac His	576
			180			185						190				
cgt Arg	ggt Gly	ggt Gly	gat Asp	ctt Leu	cgt Arg	cgt Arg	gct Ala	cgt Arg	gca Ala	gct Ala	gca Ala	gca Ala	aac Asn	atc Ile	gtt Val	624
195						200			205							
cct Pro	aac Asn	tca Ser	act Thr	ggt Gly	gct Ala	gct Ala	aaa Lys	gca Ala	atc Ile	ggt Gly	ctt Leu	gtt Val	atc Ile	cca Pro	gaa Glu	672
210						215			220							
tta Leu	aat Asn	ggt Gly	aaa Lys	ctt Leu	gac Asp	ggt Gly	gct Ala	gca Ala	caa Gln	cgt Arg	gtt Val	cct Pro	gtt Val	cca Pro	act Thr	720
225			230						235			240				
gga Gly	tca Ser	gta Val	act Thr	gaa Glu	tta Leu	gta Val	gca Ala	gtt Val	ctt Leu	gaa Glu	aaa Lys	gat Asp	act Thr	tca Ser	gta Val	768
			245						250			255				
gaa Glu	gaa Glu	atc Ile	aat Asn	gca Ala	gct Ala	atg Met	aaa Lys	gca Ala	gca Ala	gct Ala	aac Asn	gat Asp	tca Ser	tac Tyr	ggt Gly	816
			260			265			270							
tac Tyr	act Thr	gaa Glu	gat Asp	gct Ala	atc Ile	gta Val	tca Ser	tca Ser	gat Asp	atc Ile	gta Val	ggt Gly	att Ile	tct Ser	tac Tyr	864
275						280			285							
ggt Gly	tca Ser	tta Leu	ttt Phe	gat Asp	gct Ala	act Thr	caa Gln	act Thr	aaa Lys	gta Val	caa Gln	act Thr	gtt Val	gat Asp	gga Gly	912
290						295			300							
aat Asn	caa Gln	ttg Leu	gtt Val	aaa Lys	gtt Val	gtt Val	tca Ser	tgg Trp	tat Tyr	gac Asp	aat Asn	gaa Glu	atg Met	tct Ser	tac Tyr	960
305			310						315			320				

act gct caa ctt gtt cgt act ctt gag tac ttt gca aaa atc gct aaa 1008
 Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
 325 330 335

taa 1011

<210> 12

<211> 336

<212> PRT

<213> Streptococcus iniae

<400> 12

Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
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Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
 20 25 30

Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
 35 40 45

Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
 50 55 60

Phe Glu Val Asn Gly Ser Phe Val Lys Val Ser Ala Glu Arg Glu Pro
 65 70 75 80

Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Asp Ile Val Leu Glu Ala
 85 90 95

Thr Gly Phe Phe Ala Ser Lys Ala Ala Ala Glu Gln His Ile His Ala
 100 105 110

Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
 115 120 125

Lys Thr Val Val Tyr Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
 130 135 140

Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
 145 150 155 160

Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
 165 170 175

Thr Ile His Gly Tyr Thr Gly Asp Gln Met Val Leu Asp Gly Pro His
 180 185 190

Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Ala Ala Ala Asn Ile Val
 195 200 205

Pro	Asn	Ser	Thr	Gly	Ala	Ala	Lys	Ala	Ile	Gly	Leu	Val	Ile	Pro	Glu	
	210					215					220					
Leu	Asn	Gly	Lys	Leu	Asp	Gly	Ala	Ala	Gln	Arg	Val	Pro	Val	Pro	Thr	
225					230					235					240	
Gly	Ser	Val	Thr	Glu	Leu	Val	Ala	Val	Leu	Glu	Lys	Asp	Thr	Ser	Val	
				245					250					255		
Glu	Glu	Ile	Asn	Ala	Ala	Met	Lys	Ala	Ala	Ala	Asn	Asp	Ser	Tyr	Gly	
			260					265					270			
Tyr	Thr	Glu	Asp	Ala	Ile	Val	Ser	Ser	Asp	Ile	Val	Gly	Ile	Ser	Tyr	
		275					280					285				
Gly	Ser	Leu	Phe	Asp	Ala	Thr	Gln	Thr	Lys	Val	Gln	Thr	Val	Asp	Gly	
	290					295					300					
Asn	Gln	Leu	Val	Lys	Val	Val	Ser	Trp	Tyr	Asp	Asn	Glu	Met	Ser	Tyr	
305					310					315					320	
Thr	Ala	Gln	Leu	Val	Arg	Thr	Leu	Glu	Tyr	Phe	Ala	Lys	Ile	Ala	Lys	
				325					330					335		